REMARKS

Non-elected claims 21, 22 and 25 of Groups III and IV are cancelled without prejudice to the filing of divisional application thereon. The Cross-Reference to Related Applications is now amended to clarify the claim for priority.

On the issue of the lack of unity requirement, the examiner indicated in a teleconference on March 25, 2003, that the authors of the Inbal et al. reference cited by the examiner as being anticipatory to the polypeptide of Group I is not the same as the inventive entity in the present application because, even though the present inventor Adi Kimchi is a named co-author, there are additional co-authors of the reference who are not named co-inventors. This is however irrelevant as the examiner is citing Inbal et al. only for disclosure of SEQ ID NO:2 and not "at least 85% sequence identity to the amino acid sequence of SEQ ID NO:2". Accordingly, the provisional application on which priority is claimed discloses SEQ ID NO:2 and therefore eliminates Inbal et al. as a prior art reference against SEQ ID NO:2. Nevertheless, in deference to the examiner applicant intends to file an *In re Katz*-type declaration in accordance with MPEP 715.01(c) to resolve this issue, even though it is considered unnecessary.

On the issue of claims 1, 8, 20, and 27 being anticipated by Deiss et al. or Akira et al. because the examiner

asserts that Deiss teaches a DAP kinase which has 83.7% identity to residues 13-275 of SEQ ID NO:2 and that Akira teaches a murine Zip Kinase which has 82.4% identity to residues 13-275 of SEQ ID NO:2. Applicant emphasizes again that the 83.7% and 82.4% are presented for the alignments as query match, which is not sequence identity. What is shown as sequence identity on the sequence alignments provided by the examiner is the "Best Local Similarity" of 79.5% in both Deiss and Akira when aligned with residues 13-275 of SEQ ID NO:2. This is absolutely clear to those of skill in the art because the sequences in the alignment are the same length with no gaps. As pointed out in the amendment filed November 13, 2002, one can easily see that over the aligned 263 residues, there are 52 mismatched residues or in other words 209 residues that match exactly. Thus, it is unambiguous that the sequence identity is (209/263) x 100%=79.5%, which is exactly the "Best Local Similarity" given in both the Deiss and Akia sequence alignments. Without the need to compensate for gaps using a gap penalty, etc., as is the case here, all sequence comparison programs will give a sequence identity of 79.5% as can be calculated quickly and accurately even by hand. Accordingly, the 79.5% sequence identity of Deiss or Akira with residues 13-275 of SEQ ID NO:2 cannot anticipate the present claims, which recite "at least 85% sequence identity".

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Reconsideration and allowance are therefore respectfully.

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.
Attorneys for Applicant(s)

By _____
Allen C. Yun
Registration No. 37,971

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Allen C. Yun
Name

_____
Signature

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Date

ACY:pp
624 Ninth Street, N.W., Suite 300
Washington, DC 20001-5303
Telephone No.: (202) 628-5197
Facsimile No.: (202) 737-3528
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